

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	170	balint.inv.	US-PGPUB; USPAT	OR	ON	2005/10/26 11:31
L2	643	her.inv.	US-PGPUB; USPAT	OR	ON	2005/10/26 11:31
L3	8	l1 and l2	US-PGPUB; USPAT	OR	ON	2005/10/26 11:31
L4	5011	"182".clm.	US-PGPUB; USPAT	OR	ON	2005/10/26 11:31
L5	0	l3 and l4	US-PGPUB; USPAT	OR	ON	2005/10/26 11:32
L6	3929	threonine.clm.	US-PGPUB; USPAT	OR	ON	2005/10/26 11:32
L7	0	l3 and l6	US-PGPUB; USPAT	OR	ON	2005/10/26 11:32
L8	1	l1 and l6	US-PGPUB; USPAT	OR	ON	2005/10/26 11:33
L9	632	panorama.asn. or horizon.asn. or pan. asn.	US-PGPUB; USPAT	OR	ON	2005/10/26 11:34
L10	1435	l1 or l2 or l9	US-PGPUB; USPAT	OR	ON	2005/10/26 11:34
L11	1	l10 and "182".clm.	US-PGPUB; USPAT	OR	ON	2005/10/26 11:34
L12	1	l10 and threonine.clm.	US-PGPUB; USPAT	OR	ON	2005/10/26 11:35

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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:19:01 ; Search time 167 Seconds
(without alignments)
377.497 Million cell updates/sec

Title: US-09-526-106B-27_COPY_1_163

Perfect score: 842
Sequence: 1 HPETLVKVKDAEDQLGARVG.....LNEAIPIEDRDITTPVAMAT 163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

- 1: Geneseq19808:*
- 2: Geneseq19908:*
- 3: Geneseq20008:*
- 4: Geneseq20018:*
- 5: Geneseq20028:*
- 6: Geneseq20038:*
- 7: Geneseq20038:*
- 8: Geneseq20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	836	99.3	263	AAE05544	Aae05544 E. coli m
2	836	99.3	263	AAE05544	Aab36692 Escherich
3	836	99.3	263	ADJ67709	Adj67709 Escherich
4	836	99.3	264	AAW16634	AAW16634 Beta-lact
5	836	99.3	264	AAW18680	AAW18680 Intracell
6	836	99.3	286	AAAR31575	AAAR31575 Ampicilli
7	836	99.3	286	AAAR37619	AAAR37619 Secretory
8	836	99.3	286	AAAR36423	AAAR36423 Cytochrom
9	836	99.3	286	AAW16635	AAW16635 Beta-lact
10	836	99.3	286	AAW18679	AAW18679 Secretory
11	836	99.3	286	AAW08529	AAW08529 Vector PA
12	836	99.3	286	AAAB10442	AAAB10442 Expressio
13	836	99.3	286	AAAB10438	AAAB10438 Expressio
14	836	99.3	286	AAAB10440	AAAB10440 Expressio
15	836	99.3	286	AAAB50898	AAAB50898 Protein e
16	836	99.3	286	AAAB31173	AAAB31173 Amino aci
17	836	99.3	286	AAU75551	AAU75551 celz inte
18	836	99.3	286	ADP55474	ADP55474 Vector PC
19	836	99.3	286	ABR43622	ABR43622 Cloning v
20	836	99.3	286	ADR70422	ADR70422 Vector PA
21	836	99.3	286	ADR70410	ADR70410 Vector PA
22	836	99.3	286	ADR70404	ADR70404 Vector PA
23	836	99.3	286	ADR70416	ADR70416 Vector PA
24	836	99.3	286	ADR70428	ADR70428 Vector PA
25	836	99.3	290	AAU23219	AAU23219 Novel hum

26	836	99.3	290	4	AAW84362	Human imm
27	836	99.3	327	2	AAW16636	Beta-lact
28	836	99.3	327	2	AAW18681	Membrane
29	836	99.3	408	6	ABR55981	hCG beta-
30	836	99.3	585	6	ADA67747	Beta-lact
31	836	99.3	1031	5	ADI46109	Single st
32	836	99.3	1088	2	AAE88636	Plasmid p
33	836	99.3	1277	2	AAE52701	Plasmid p
34	836	99.3	2307	3	AAI70064	Recombina
35	836	99.3	2307	3	AAI70065	Recombina
36	836	99.3	2307	3	AAI70066	Recombina
37	836	99.3	2761	2	ADH11249	Vertebra
38	835	99.2	286	2	AAW06551	Escherich
39	835	99.2	872	7	ADK65686	E coli cl
40	835	99.2	1293	7	ADH14284	Human Gp
41	835	99.2	1293	7	ADH14284	Vector PC
42	835	99.2	1967	6	ABR82793	Amino aci
43	833	98.9	286	5	ADJ31652	Klebsiell
44	833	98.9	286	6	ADA67741	K. pneumo
45	833	98.9	583	6	ADA67745	Beta-lact

ALIGNMENTS

RESULT 1
AAE05544
ID AAE05544 standard; protein; 263 AA.

XX AAE05544;

DT 24-SEP-2001 (first entry)

XX E. coli mature TEM-1 beta-lactamase.

XX Interaction-dependent enzyme association; IDSA system; biosensor;
circularly permuted interaction-activated protein; marker protein;
type A beta-lactamase; TEM-1 beta-lactamase; protein-protein interaction;
therapeutic; drug screening; thioredoxin; ampicillin resistance.

OS Escherichia coli.

PH Key Location/Qualifiers

FT Cleavage-site 27..28 /note= "Break-point between alpha and omega fragments"

FT Region 36..40 /note= "Inter-sub-domain loop"

FT Cleavage-site 38..39 /note= "Break-point between alpha and omega fragments"

FT Active-site 45

FT Cleavage-site 74..75 /note= "Break-point between alpha and omega fragments"

FT Cleavage-site 149..150 /note= "Break-point between alpha and omega fragments"

FT Cleavage-site 172..173 /note= "Break-point between alpha and omega fragments"

FT Region 189..204 /note= "Inter-sub-domain loop"

FT Cleavage-site 190..191 /note= "Break-point between alpha and omega fragments"

FT Cleavage-site 202..203 /note= "Break-point between alpha and omega fragments"

FT Cleavage-site 228..229 /note= "Break-point between alpha and omega fragments"

XX WO200151629-A2.

PN 19-JUL-2001.

PD 16-JAN-2001; 2001WO-US001651.

PF 13-JAN-2000; 2000US-0175968P.

PR 15-MAR-2000; 2000US-00526106.

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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:20:11 ; Search time 16 Seconds
(without alignments)
980.208 Million cell updates/sec

Title: US-09-526-106b-27_COPY_1_163

Perfect score: 842
Sequence: 1 HPETLVKVDADQLGARVG.....LNEALPNDERTTTPVAMAT 163

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

PIR 79:*

1: Pirl:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	836	99.3	286	2 T51301	Beta-lactamase (EC
2	836	99.3	286	2 S47061	Beta-lactamase (EC
3	836	99.3	286	4 S41975	Beta-lactamase (EC
4	831	98.7	286	1 NPECP	Beta-lactamase (EC
5	831	98.7	286	4 I40905	Beta-lactamase (EC
6	823	97.7	286	2 S30113	Beta-lactamase (EC
7	818	97.1	286	2 S60312	extended spectrum
8	817	97.0	286	2 S60310	Beta-lactamase (EC
9	817	97.0	286	2 S60311	Bla protein - Salm
10	817	97.0	286	2 JQ1546	Beta-lactamase (EC
11	800	71.3	286	2 S16146	Beta-lactamase (EC
12	600	71.3	286	2 A60679	Beta-lactamase (EC
13	596	70.8	265	2 S00464	Beta-lactamase (EC
14	596	70.8	265	2 S02434	Beta-lactamase (EC
15	596	70.8	265	2 A60448	Beta-lactamase (EC
16	596	70.8	286	1 A44998	Beta-lactamase (EC
17	596	70.8	286	2 A60632	Beta-lactamase (EC
18	596	70.8	286	2 A37200	Beta-lactamase (EC
19	590	70.1	287	1 A44996	Beta-lactamase (EC
20	575	68.3	279	2 A24469	Beta-lactamase (EC
21	545	64.7	286	1 A44958	Beta-lactamase (EC
22	463	55.0	298	2 A41381	Beta-lactamase (EC
23	375.5	44.6	314	2 S06967	Beta-lactamase (EC
24	370.5	44.0	302	2 S36188	Beta-lactamase (EC
25	367.5	43.6	306	2 G69674	probable Beta lact
26	366.5	43.5	281	2 D95395	Beta-lactamase (EC
27	365.5	43.4	294	2 S16553	Beta-lactamase (EC
28	358.5	42.6	263	2 A54543	Beta-lactamase (EC
29	356.5	42.3	306	1 B45822	Beta-lactamase (EC

30	356	42.3	305	2 A61156	Beta-lactamase (EC
31	356	42.3	305	2 A57002	Beta-lactamase (EC
32	356	42.3	305	2 A60680	Beta-lactamase (EC
33	355.5	42.2	291	2 S42075	Beta-lactamase (EC
34	355.5	42.2	306	2 S47330	penicillinase - Ba
35	353	41.9	293	2 S04649	Beta-lactamase (EC
36	352.5	41.9	311	2 JN0520	Beta-lactamase (EC
37	340.5	40.4	305	1 C45822	Beta-lactamase (EC
38	340	40.4	310	2 JF0091	Beta-lactamase (EC
39	337.5	40.1	291	2 JF0074	Beta-lactamase (EC
40	337	40.0	294	2 S44080	Beta-lactamase (EC
41	332.5	39.5	306	1 PNBSSB	Beta-lactamase (EC
42	332.5	39.5	306	1 PNBSSU	Beta-lactamase (EC
43	332.5	39.5	306	2 S03167	Beta-lactamase (EC
44	332	39.4	314	1 PNSM1U	Beta-lactamase (EC
45	331.5	39.4	307	1 PNBSL	Beta-lactamase (EC

ALIGNMENTS

RESULT 1

T51301
beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C:Accession: T51301
R:WACH, A.; BRACHAT, A.; ALBERTISEGUI, C.; REBISCHUNG, C.; PHILIPPSEN, P.
Yeast 13, 1065-1075, 1997
A:Title: Heterologous HIS3 marker and GFP reporter modules for PCR-targeting in Saccharom
A:Reference number: Z09587
A:Accession: T51301
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-286 <WAC>
A:Cross-references: EMBL:AJ002683; PIDN:CAA05686.1
C:Genetics:
A:Gene: bla
C:Superfamily: beta-lactamase I
C:Keywords: hydrolase

Query Match 99.3%; Score 836; DB 2; Length 286;
Best Local Similarity 99.4%; Pred. No. 7.1e-71;
Matches 162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	HPETLVKVDADQLGARVGYIELDLSKILLESFPERFPMWSTFKVLLCGAVLSRID 60
DB	24	HPETLVKVDADQLGARVGYIELDLSKILLESFPERFPMWSTFKVLLCGAVLSRID 83
QY	61	AGQEQIGRIHYSONDLVEYSPVTEKHLTDGMTVRLCSAAITMSDNTAANLLLTIGGP 120
DB	84	AGQEQIGRIHYSONDLVEYSPVTEKHLTDGMTVRLCSAAITMSDNTAANLLLTIGGP 143
QY	121	KEITAFIHNMGDHTVRLDRWPELNEAIPNDRDITTPVAMAT 163
DB	144	KEITAFIHNMGDHTVRLDRWPELNEAIPNDRDITTPVAMAT 186

RESULT 2

S47061
beta-lactamase (EC 3.5.2.6) - phage phi-X174
C:Species: phage phi-X174
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S47061
R:Henrich, B.; Schmidtberger, B.
submitted to the EMBL Data Library, July 1994
A:Description: A variant of phiX174 gene E-based positive selection vectors with enhance
A:Reference number: S47060
A:Accession: S47061
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <HEN>
A:Cross-references: UNIPROT:Q38058; EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g52091

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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:12:30 ; Search time 60 Seconds
(without alignments)
1391.148 Million cell updates/sec

Title: US-09-526-106B-27_COPY_1_163

Perfect score: 842
Sequence: 1 HPETLVKVKDAEDQLGARVG.....LNEAIPNDERDITTPVAMAT 163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	837	99.4	286	2 Q8KMX4	Q8KMX4 escherichia
2	837	99.4	286	2 Q6ZYM6	Q6ZYM6 salmonella
3	837	99.4	286	2 Q9R748	Q9R748 klebsiella
4	836	99.3	229	2 Q6WY75	Q6WY75 klebsiella
5	836	99.3	232	2 Q6WY74	Q6WY74 hafnia alve
6	836	99.3	241	2 Q6WY78	Q6WY78 klebsiella
7	836	99.3	242	2 Q6WY73	Q6WY73 escherichia
8	836	99.3	285	2 Q6KB67	Q6KB67 hordeum vul
9	836	99.3	286	2 Q38058	Q38058 bacterioph
10	836	99.3	286	2 Q00626	Q00626 staphylococ
11	836	99.3	286	2 Q79CL6	Q79CL6 methylobaci
12	836	99.3	286	2 Q79DR3	Q79DR3 escherichia
13	833	98.9	279	2 Q9X5K9	Q9X5K9 salmonella
14	833	98.9	285	2 Q6EH43	Q6EH43 morganelia
15	833	98.9	286	2 Q8KMX3	Q8KMX3 escherichia
16	833	98.9	286	2 Q8KQ72	Q8KQ72 escherichia
17	833	98.9	286	2 Q6IT48	Q6IT48 escherichia
18	833	98.9	286	2 Q7BQ65	Q7BQ65 proteus mir
19	833	98.9	286	2 Q9AEY6	Q9AEY6 klebsiella
20	833	98.9	286	2 Q9LAC0	Q9LAC0 proteus mir
21	833	98.9	286	2 Q9A429	Q9A429 morganelia
22	833	98.9	286	2 Q9R435	Q9R435 klebsiella
23	831	98.7	225	2 Q38212	Q38212 bacterioph
24	831	98.7	232	2 Q6PRU7	Q6PRU7 escherichia
25	831	98.7	255	2 Q84H50	Q84H50 escherichia
26	831	98.7	261	2 Q84H49	Q84H49 klebsiella
27	831	98.7	264	2 Q6PRU6	Q6PRU6 acinetobact
28	831	98.7	281	2 Q6QIV0	Q6QIV0 serratia ma
29	831	98.7	282	2 Q6QIV1	Q6QIV1 serratia ma
30	831	98.7	286	1 BLAT_ECOLI	P62593 escherichia
31	831	98.7	286	1 BLAT_SALTI	P62594 salmonella

32	831	98.7	286	2 O53043	O53043 klebsiella
33	831	98.7	286	2 O8KSD3	O8KSD3 klebsiella
34	831	98.7	286	2 O8VP43	O8VP43 klebsiella
35	831	98.7	286	2 Q933Z8	Q933Z8 escherichia
36	831	98.7	286	2 Q934D7	Q934D7 escherichia
37	831	98.7	286	2 Q93477	Q93477 escherichia
38	831	98.7	286	2 Q93G13	Q93G13 klebsiella
39	831	98.7	286	2 Q6A253	Q6A253 haemophilus
40	831	98.7	286	2 Q6LBN9	Q6LBN9 pseudomonas
41	831	98.7	286	2 Q6LCV6	Q6LCV6 neisseria g
42	831	98.7	286	2 Q6TWH1	Q6TWH1 streptococ
43	831	98.7	286	2 Q6UVM7	Q6UVM7 acinetobact
44	831	98.7	286	2 Q6W7J4	Q6W7J4 escherichia
45	831	98.7	286	2 Q6W9J1	Q6W9J1 enterobacte

ALIGNMENTS

RESULT 1
Q8KMX4 PRELIMINARY; PRT; 286 AA.
ID AC Q8KMX4;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE TEM-93 ES-Beta-lactamase.
GN Name=bla-TEM-93;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLSIS 3445/98;
RA Baraniak A.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLSIS 3445/98;
RA Gniadkowski M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ318093; CAC85660.1; -
DR HSP; Q9R435; IHTZ.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; Beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Plasmid.
SQ SEQUENCE 286 AA; 31514 MW; 1555DCE499016FB8 CRC64;

Query Match 99.4%; Score 837; DB 2; Length 286;
Best Local Similarity 98.8%; Pred. No. 1.le-65;
Matches 161; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	HPETLVKVKDAEDQLGARVG	YIELDNSGKILSFRPEERFPM	STFKVLCGAVLSRID	60
Db	24	HPETLVKVKDAEDQLGARVG	YIELDNSGKILSFRPEERFPM	STFKVLCGAVLSRVD	83
Qy	61	AGQELGRRIRHYSONDLVE	YSPVTEKHLTGQMTVRELCS	AAITMSDNTAANLLTTGGP	120
Db	84	AGQELGRRIRHYSONDLVE	YSPVTEKHLTGQMTVRELCS	AAITMSDNTAANLLTTGGP	143
Qy	121	KELTAFLNMGDGHVTRLD	RWPELNEAIPNDERDITTP	VAMAT	163
Db	144	KELTAFLNMGDGHVTRLD	RWPELNEAIPNDERDITTP	VAMAT	186

RESULT 2
Q6ZYM6 PRELIMINARY; PRT; 286 AA.
ID Q6ZYM6

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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:22:11 ; Search time 22 Seconds
(without alignments)
553.082 Million cell updates/sec

Title: US-09-526-106B-27_COPY_1_163
Perfect score: 842
Sequence: 1 HPETLVKVKDAEDQLGARVGYIELDLNSGKILSPFRPEPPMSTFKVLLCGAVLSRID 163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/protdata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/protdata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/protdata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/protdata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/protdata/1/iaa/PCUTS_COMB.pep.*
6: /cgn2_6/protdata/1/iaa/backfiles.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	836	99.3	286	1	US-07-721-775A-2
2	836	99.3	286	1	US-08-339-658-2
3	836	99.3	286	3	US-09-263-933-7
4	836	99.3	286	3	US-09-263-933-14
5	836	99.3	286	3	US-09-263-933-21
6	836	99.3	286	3	US-09-025-769B-265
7	836	99.3	286	3	US-09-025-769B-362
8	836	99.3	286	4	US-09-919-901-7
9	836	99.3	286	4	US-09-919-901-14
10	836	99.3	286	4	US-09-919-901-21
11	836	99.3	286	4	US-09-490-070A-265
12	836	99.3	286	4	US-09-490-070A-362
13	836	99.3	286	4	US-09-490-153-265
14	836	99.3	286	4	US-09-490-153-362
15	836	99.3	286	4	US-10-191-966-7
16	836	99.3	286	4	US-10-191-966-14
17	836	99.3	286	4	US-10-191-966-21
18	836	99.3	286	4	US-09-490-324-265
19	836	99.3	286	4	US-09-490-324-362
20	836	99.3	299	3	US-09-025-769B-285
21	836	99.3	299	3	US-09-025-769B-298
22	836	99.3	299	3	US-09-025-769B-300
23	836	99.3	299	4	US-09-490-070A-285
24	836	99.3	299	4	US-09-490-070A-298
25	836	99.3	299	4	US-09-490-070A-300
26	836	99.3	299	4	US-09-490-153-285
27	836	99.3	299	4	US-09-490-153-298

28	836	99.3	299	4	US-09-490-153-300	Sequence 300, App
29	836	99.3	299	4	US-09-490-324-285	Sequence 285, App
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31	836	99.3	299	4	US-09-490-324-300	Sequence 300, App
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33	836	99.3	2307	3	US-09-263-933-9	Sequence 9, Appl1
34	836	99.3	2307	3	US-09-263-933-16	Sequence 16, Appl1
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38	836	99.3	2307	4	US-10-191-966-2	Sequence 2, Appl1
39	836	99.3	2307	4	US-10-191-966-9	Sequence 9, Appl1
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45	831	98.7	263	1	US-08-407-544-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-07-721-775A-2
; Sequence 2, Application US/07721775A
; Patent No. 5180666
; GENERAL INFORMATION:
; APPLICANT: States, J. Christopher
; APPLICANT: Hines, Ronald N.
; APPLICANT: No. 5180666ak, Raymond F.
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
; TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Echington, Barnard, Perry & Milton
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48099
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/721,775A
; FILING DATE: 19910627
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-321WSU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; TELEFAX: (313) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-721-775A-2

Query Match 99.3%; Score 836; DB 1; Length 286;

Best Local Similarity 99.4%; Pred. No. 7e-91; Indels 0; Gaps 0;
Matches 162; Conservative 0; Mismatches 1;

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DB 24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILSPFRPEPPMSTFKVLLCGAVLSRID 83

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OM protein - protein search, using sw model

Run on: October 26, 2005, 05:29:12 ; Search time 68 Seconds
(without alignments)
1000.798 Million cell updates/sec

Title: US-09-526-106b-27_COPY_1_163

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	836	99.3	286	10	US-09-919-901-7
3	836	99.3	286	10	US-09-919-901-14
4	836	99.3	286	10	US-09-919-901-21
5	836	99.3	286	11	US-09-837-306-354
6	836	99.3	286	14	US-10-191-966-7
7	836	99.3	286	14	US-10-191-966-14
8	836	99.3	286	14	US-10-191-966-21
9	836	99.3	286	15	US-10-045-674-523
10	836	99.3	286	16	US-10-416-708A-73
11	836	99.3	2307	10	US-09-919-901-2

12	836	99.3	2307	10	US-09-919-901-9	Sequence 9, Appli
13	836	99.3	2307	10	US-09-919-901-16	Sequence 16, Appli
14	836	99.3	2307	14	US-10-191-966-2	Sequence 2, Appli
15	836	99.3	2307	14	US-10-191-966-9	Sequence 9, Appli
16	836	99.3	2307	14	US-10-191-966-16	Sequence 16, Appli
17	835	99.2	286	14	US-10-231-013-9	Sequence 9, Appli
18	835	99.2	286	16	US-10-842-534-9	Sequence 9, Appli
19	835	99.2	1293	14	US-10-251-385-292	Sequence 292, Appli
20	835	99.2	1293	18	US-10-668-035-57	Sequence 57, Appli
21	835	99.2	1967	16	US-10-477-044-1	Sequence 1, Appli
22	831	98.7	265	9	US-09-772-114-6	Sequence 6, Appli
23	831	98.7	265	14	US-10-280-482-2	Sequence 2, Appli
24	831	98.7	265	17	US-10-656-029-2	Sequence 2, Appli
25	831	98.7	285	9	US-09-772-114-7	Sequence 7, Appli
26	831	98.7	286	14	US-10-016-668-5	Sequence 5, Appli
27	831	98.7	286	14	US-10-280-482-4	Sequence 4, Appli
28	831	98.7	286	17	US-10-656-029-4	Sequence 4, Appli
29	831	98.7	286	17	US-10-877-952-26	Sequence 26, Appli
30	831	98.7	286	17	US-10-877-952-71	Sequence 71, Appli
31	831	98.7	286	20	US-11-059-226-34	Sequence 34, Appli
32	831	98.7	286	20	US-11-059-226-36	Sequence 35, Appli
33	831	98.7	286	20	US-11-059-226-36	Sequence 36, Appli
34	831	98.7	673	18	US-10-450-763-58554	Sequence 58554, A
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36	828	98.3	364	17	US-10-877-952-18	Sequence 18, Appli
37	828	98.3	362	15	US-10-469-199-2	Sequence 2, Appli
38	828	98.3	584	17	US-10-890-675-2	Sequence 2, Appli
39	824	97.9	265	9	US-09-772-114-8	Sequence 8, Appli
40	824	97.9	265	14	US-10-280-482-6	Sequence 6, Appli
41	824	97.9	265	16	US-10-622-088-114	Sequence 114, Appli
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43	824	97.9	265	17	US-10-877-952-154	Sequence 154, Appli
44	824	97.9	265	20	US-11-040-924-1	Sequence 1, Appli
45	823	97.7	264	9	US-09-772-114-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-668-778-2
; Sequence 2, Application US/10668778
; Publication No. US20040038317A1
; GENERAL INFORMATION:
; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Hong
; APPLICANT: Kalobios, Inc.
; TITLE OF INVENTION: Interaction-Activated Proteins
; FILE REFERENCE: 021167-00070005
; CURRENT APPLICATION NUMBER: US/10/668, 778
; CURRENT FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: US/09/526,106
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 60/124,339
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: US 60/135,926
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/175,968
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; OTHER INFORMATION: TEM-1 beta-lactamase
US-10-668-778-2

Query Match 99.3%; Score 836; DB 15; Length 263;
Best Local Similarity 99.4%; Pred. No. 7,8e-83;
Matches 162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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